_Crouch_
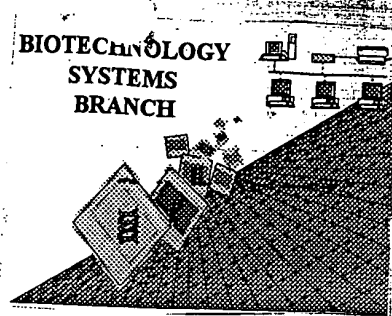
# RAW SEQUENCE LISTING
# ERROR REPORT

#3

12/29/00

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/662,128_

Source: _1632_

Date Processed by STIC: _12/13/2000_

**RECEIVED**

DEC 2 8 2000

TECH CENTER 1600/2900

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**
**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**
**PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)**
**PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

## Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
**http://www.uspto.gov/web/offices/pac/checker**

1632

```
RAW SEQUENCE LISTING            DATE: 12/13/2000
PATENT APPLICATION:  US/09/662,128     TIME: 10:41:39

      Input Set : A:\19733US0.txt
      Output Set: N:\CRF3\12132000\I662128.raw
```

**Does Not Comply**
**Corrected Diskette Needed**

*pp 1-4*

```
 3 <110> APPLICANT: MIYAGAWA, SHUJI
 4         OKABE, MASARU
 6 <120> TITLE OF INVENTION: MODIFIED CRE RECOMBINASE GENE FOR MAMMALS
 8 <130> FILE REFERENCE: 197330US0
10 <140> CURRENT APPLICATION NUMBER: 09/662,128
11 <141> CURRENT FILING DATE: 2000-09-14
13 <150> PRIOR APPLICATION NUMBER: JP11-264364
14 <151> PRIOR FILING DATE: 1999-09-17
16 <160> NUMBER OF SEQ ID NOS: 6
18 <170> SOFTWARE: PatentIn version 3.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1050
22 <212> TYPE: DNA
23 <213> ORGANISM: Artificial/Unknown
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(1050)
29 <220> FEATURE:
30 <221> NAME/KEY: misc_feature
31 <222> LOCATION: ()..()
32 <223> OTHER INFORMATION: Description of Artificial Sequence: gene
35 <400> SEQUENCE: 1
```

*Per 1.823 of new Sequence Rules,*
*<213> response is either Unknown,*
*Artificial Sequence, OR*
*scientific name*
*(Genus/species)*

*one of the above*

*Since <213> response*
*is "Description of*
*Artificial Sequence,"*
*use Artificial Sequence*
*as <213> response.*

```
36 atg ccc aag aag aag agg aag gtg agc aac ctg ctg acc gtg cac cag     48
37 Met Pro Lys Lys Lys Arg Lys Val Ser Asn Leu Leu Thr Val His Gln
38 1               5                   10                  15
40 aac ctg ccc gcc ctg ccc gtg gac gcc acc agc gac gag gtg cgc aag     96
41 Asn Leu Pro Ala Leu Pro Val Asp Ala Thr Ser Asp Glu Val Arg Lys
42             20                  25                  30
44 aac ctg atg gac atg ttc cgc gac cgc cag gcc ttc agc gag cac acc    144
45 Asn Leu Met Asp Met Phe Arg Asp Arg Gln Ala Phe Ser Glu His Thr
46             35                  40                  45
48 tgg aag atg ctg ctg agc gtg tgc cgc agc tgg gcc gcc tgg tgc aag    192
49 Trp Lys Met Leu Leu Ser Val Cys Arg Ser Trp Ala Ala Trp Cys Lys
50     50                  55                  60
52 ctg aac aac cgc aag tgg ttc ccc gcc gag ccc gag gac gtg cgc gac    240
53 Leu Asn Asn Arg Lys Trp Phe Pro Ala Glu Pro Glu Asp Val Arg Asp
54 65                  70                  75                  80
56 tac ctg ctg tac ctg cag gcc cgc ggc ctg gcc gtg aag acc atc cag    288
57 Tyr Leu Leu Tyr Leu Gln Ala Arg Gly Leu Ala Val Lys Thr Ile Gln
58                 85                  90                  95
60 cag cac ctg ggc cag ctg aac atg ctg cac cgc cgc agc ggc ctg ccc    336
61 Gln His Leu Gly Gln Leu Asn Met Leu His Arg Arg Ser Gly Leu Pro
62             100                 105                 110
64 cgc ccc agc gac agc aac gcc gtg agc ctg gtg atg cgc cgc atc cgc    384
65 Arg Pro Ser Asp Ser Asn Ala Val Ser Leu Val Met Arg Arg Ile Arg
66             115                 120                 125
68 aag gag aac gtg gac gcc ggc gag cgc gcc aag cag gcc ctg gcc ttc    432
```

```
 69 Lys Glu Asn Val Asp Ala Gly Glu Arg Ala Lys Gln Ala Leu Ala Phe
 70         130                 135                 140
 72 gag cgc acc gac ttc gac cag gtg cgc agc ctg atg gag aac agc gac    480
 73 Glu Arg Thr Asp Phe Asp Gln Val Arg Ser Leu Met Glu Asn Ser Asp
 74 145                 150                 155                 160
 76 cgc tgc cag gac atc cgc aac ctg gcc ttc ctg ggc atc gcc tac aac    528
 77 Arg Cys Gln Asp Ile Arg Asn Leu Ala Phe Leu Gly Ile Ala Tyr Asn
 78                 165                 170                 175
 80 acc ctg ctg cgc atc gcc gag atc gcc cgc atc cgc gtg aag gac atc    576
 81 Thr Leu Leu Arg Ile Ala Glu Ile Ala Arg Ile Arg Val Lys Asp Ile
 82             180                 185                 190
 84 agc cgc acc gac ggc ggc cgc atg ctg atc cac atc ggc cgc acc aag    624
 85 Ser Arg Thr Asp Gly Gly Arg Met Leu Ile His Ile Gly Arg Thr Lys
 86             195                 200                 205
 88 acc ctg gtg agc acc gcc ggc gtg gag aag gcc ctg agc ctg ggc gtg    672
 89 Thr Leu Val Ser Thr Ala Gly Val Glu Lys Ala Leu Ser Leu Gly Val
 90     210                 215                 220
 92 acc aag ctg gtg gag cgc tgg atc agc gtg agc ggc gtg gcc gac gac    720
 93 Thr Lys Leu Val Glu Arg Trp Ile Ser Val Ser Gly Val Ala Asp Asp
 94 225                 230                 235                 240
 96 ccc aac aac tac ctg ttc tgc cgc gtg cgc aag aac ggc gtg gcc gcc    768
 97 Pro Asn Asn Tyr Leu Phe Cys Arg Val Arg Lys Asn Gly Val Ala Ala
 98                 245                 250                 255
100 ccc agc gcc acc agc cag ctg agc acc cgg gcc ctg gag ggc atc ttc    816
101 Pro Ser Ala Thr Ser Gln Leu Ser Thr Arg Ala Leu Glu Gly Ile Phe
102             260                 265                 270
104 gag gcc acc cac cgc ctg atc tac ggc gcc aag gac gac agc ggc cag    864
105 Glu Ala Thr His Arg Leu Ile Tyr Gly Ala Lys Asp Asp Ser Gly Gln
106             275                 280                 285
108 cgc tac ctg gcc tgg agc ggc cac agc gcc cgc gtg ggc gcc gcc cgc    912
109 Arg Tyr Leu Ala Trp Ser Gly His Ser Ala Arg Val Gly Ala Ala Arg
110     290                 295                 300
112 gac atg gcc cgc gcc ggc gtg agc atc ccc gag atc atg cag gcc ggc    960
113 Asp Met Ala Arg Ala Gly Val Ser Ile Pro Glu Ile Met Gln Ala Gly
114 305                 310                 315                 320
116 ggc tgg acc aac gtg aac atc gtg atg aac tac atc cgc aac ctg gac   1008
117 Gly Trp Thr Asn Val Asn Ile Val Met Asn Tyr Ile Arg Asn Leu Asp
118                 325                 330                 335
120 agc gag acc ggc gcc atg gtg cgc ctg ctg gag gac ggc gac          1050
121 Ser Glu Thr Gly Ala Met Val Arg Leu Leu Glu Asp Gly Asp
122             340                 345                 350
125 <210> SEQ ID NO: 2
126 <211> LENGTH: 350
127 <212> TYPE: PRT
128 <213> ORGANISM: Artificial/Unknown
130 <220> FEATURE:
131 <221> NAME/KEY: misc_feature
132 <222> LOCATION: ()..()
133 <223> OTHER INFORMATION: Description of Artificial Sequence: gene
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/662,128

DATE: 12/13/2000
TIME: 10:41:39

Input Set : A:\19733US0.txt
Output Set: N:\CRF3\12132000\I662128.raw

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135 <400> SEQUENCE: 2
137 Met Pro Lys Lys Lys Arg Lys Val Ser Asn Leu Leu Thr Val His Gln
138 1               5                   10                  15
141 Asn Leu Pro Ala Leu Pro Val Asp Ala Thr Ser Asp Glu Val Arg Lys
142             20                  25                  30
145 Asn Leu Met Asp Met Phe Arg Asp Arg Gln Ala Phe Ser Glu His Thr
146         35                  40                  45
149 Trp Lys Met Leu Leu Ser Val Cys Arg Ser Trp Ala Ala Trp Cys Lys
150     50                  55                  60
153 Leu Asn Asn Arg Lys Trp Phe Pro Ala Glu Pro Glu Asp Val Arg Asp
154 65                  70                  75                  80
157 Tyr Leu Leu Tyr Leu Gln Ala Arg Gly Leu Ala Val Lys Thr Ile Gln
158             85                  90                  95
161 Gln His Leu Gly Gln Leu Asn Met Leu His Arg Arg Ser Gly Leu Pro
162             100                 105                 110
165 Arg Pro Ser Asp Ser Asn Ala Val Ser Leu Val Met Arg Arg Ile Arg
166         115                 120                 125
169 Lys Glu Asn Val Asp Ala Gly Glu Arg Ala Lys Gln Ala Leu Ala Phe
170     130                 135                 140
173 Glu Arg Thr Asp Phe Asp Gln Val Arg Ser Leu Met Glu Asn Ser Asp
174 145                 150                 155                 160
177 Arg Cys Gln Asp Ile Arg Asn Leu Ala Phe Leu Gly Ile Ala Tyr Asn
178             165                 170 .               175
181 Thr Leu Leu Arg Ile Ala Glu Ile Ala Arg Ile Arg Val Lys Asp Ile
182             180                 185                 190
185 Ser Arg Thr Asp Gly Gly Arg Met Leu Ile His Ile Gly Arg Thr Lys
186         195                 200                 205
189 Thr Leu Val Ser Thr Ala Gly Val Glu Lys Ala Leu Ser Leu Gly Val
190     210                 215                 220
193 Thr Lys Leu Val Glu Arg Trp Ile Ser Val Ser Gly Val Ala Asp Asp
194 225                 230                 235                 240
197 Pro Asn Asn Tyr Leu Phe Cys Arg Val Arg Lys Asn Gly Val Ala Ala
198             245                 250                 255
201 Pro Ser Ala Thr Ser Gln Leu Ser Thr Arg Ala Leu Glu Gly Ile Phe
202         260                 265                 270
205 Glu Ala Thr His Arg Leu Ile Tyr Gly Ala Lys Asp Asp Ser Gly Gln
206         275                 280                 285
209 Arg Tyr Leu Ala Trp Ser Gly His Ser Ala Arg Val Gly Ala Ala Arg
210     290                 295                 300
213 Asp Met Ala Arg Ala Gly Val Ser Ile Pro Glu Ile Met Gln Ala Gly
214 305                 310                 315                 320
217 Gly Trp Thr Asn Val Asn Ile Val Met Asn Tyr Ile Arg Asn Leu Asp
218             325                 330                 335
221 Ser Glu Thr Gly Ala Met Val Arg Leu Leu Glu Asp Gly Asp
222         340                 345                 350
225 <210> SEQ ID NO: 3
226 <211> LENGTH: 34
227 <212> TYPE: DNA
228 <213> ORGANISM: Artificial/Unknown
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                RAW SEQUENCE LISTING              DATE: 12/13/2000
                PATENT APPLICATION:  US/09/662,128    TIME: 10:41:39

                Input Set : A:\19733US0.txt
                Output Set: N:\CRF3\12132000\I662128.raw

230 <220> FEATURE:
231 <221> NAME/KEY: misc_feature
232 <222> LOCATION: ()..()
233 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
236 <400> SEQUENCE: 3
237 ataacttcgt atagcataca ttatacgaag ttat                              34
240 <210> SEQ ID NO: 4
241 <211> LENGTH: 29
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial/Unknown
245 <220> FEATURE:
246 <221> NAME/KEY: misc_feature
247 <222> LOCATION: ()..()
248 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
251 <400> SEQUENCE: 4
252 ttcgtatagc atagattata cgaagttat                                    29
255 <210> SEQ ID NO: 5
256 <211> LENGTH: 29
257 <212> TYPE: DNA
258 <213> ORGANISM: Artificial/Unknown
260 <220> FEATURE:
261 <221> NAME/KEY: misc_feature
262 <222> LOCATION: ()..()
263 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
266 <400> SEQUENCE: 5
267 ataacttcgt atagcataca ttatacgaa                                    29
270 <210> SEQ ID NO: 6
271 <211> LENGTH: 21
272 <212> TYPE: DNA
273 <213> ORGANISM: Artificial/Unknown
275 <220> FEATURE:
276 <221> NAME/KEY: misc_feature
277 <222> LOCATION: ()..()
278 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
281 <400> SEQUENCE: 6
282 cccaagaaga agaggaaggt g                                            21
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VERIFICATION SUMMARY                         DATE: 12/13/2000
PATENT APPLICATION:   US/09/662,128          TIME: 10:41:40

Input Set : A:\19733US0.txt
Output Set: N:\CRF3\12132000\I662128.raw